



SEQUENCE LISTING

<110> Eck, Jorgen
Schmidt, Arno
Zinke, Holger

<120> Recombinant Fusion Proteins Based on
Ribosome-Inactivating Proteins of the mistletoe Viscum
album

Subcs
<130> 09282-5

<140> 09/347,064

<141> 1999-07-02

<150> PCT/EP98/00009

<151> 1998-01-02

<150> EP 97 10 0012.0

<151> 1997-01-02

<160> 38

<170> PatentIn Ver. 2.1

<210> 1

<211> 762

<212> DNA

<213> Viscum album

<400> 1

catatgtacg aacgtatccg tctgctgttt acccaccaga ccaccggtga agaataatttc 60
cggttcatca cgtttctccg agattatgtc tcaagcggaa gcttttccaa tgagatacca 120
ctcttgctgc agtctacgat ccccgctctcc gatgcgcaaa gatttgtctt ggtggagctc 180
accaaccagg ggggagactc gatcacggcc gccatcgacg ttaccaatct gtacgtcgtg 240
gcttaccaag caggcgacca atcctacttt ttgcgcgacg caccacgcgg cgcggaaacg 300
catctcttca ccggcaccac ccgatcctct ctcccattca acggaagcta ccctgatctg 360
gagcgatacg ccggacatag ggaccagatc cctctcggtg tagaccaact cattcaatcc 420
gtcacggcgc ttcgttttcc gggcggcagc acgcgtaccc aagctcgttc gatttttaatc 480
ctcattcaga tgatctccga ggccgccaga ttcaatccca tcttatggag ggctcgccaa 540
tacattaaca gtggggcgtc atttctgccg gacgtgtaca tgctggagct ggagacgagt 600
tgggggccaac aatccacgca agtccagcat tcaaccgatg gcgtttttta taacccaatt 660
cgggttgcta tcccccccg taacttcgtg acgttgacca atgttcgcga cgtgatcgcc 720
agcttgccga tcatgttggt tgtatgcgga gagcggccga gt 762

<210> 2

<211> 252

<212> PRT

<213> Viscum album

<400> 2

Met Tyr Glu Arg Ile Arg Leu Arg Val Thr His Gln Thr Thr Gly Glu
1 5 10 15
Glu Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly
20 25 30
Ser Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val
35 40 45
Ser Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly
50 55 60
Asp Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala
65 70 75 80
Tyr Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly
85 90 95
Ala Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe
100 105 110
Asn Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln
115 120 125
Ile Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg
130 135 140
Phe Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu
145 150 155 160
Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg
165 170 175
Ala Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr
180 185 190
Met Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln
195 200 205
His Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro
210 215 220
Pro Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser
225 230 235 240

Leu Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro
 245 250

<210> 3
 <211> 828
 <212> DNA
 <213> Viscum album

<400> 3
 aggcctgtga tagccgatga tggtacatgt agtgcttcgg aacctacggt gcggattgtg 60
 ggtcgaaatg gcatgtgctg ggacgtccga gatgacgatt tccgcgatgg aaatcagata 120
 cagttgtggc cctccaagtc caacaatgat ccgaatcagt tgtggacgat caaaagggat 180
 ggaaccattc gatccaatgg cagctgcttg accacgtatg gctatactgc tggcgtctat 240
 gtgatgatct tcgactgtaa tactgtgtgt cgggaggcca ctctttggca gatatggggc 300
 aatgggacca tcatcaatcc aagatccaat ctggttttgg cagcatcatc tggaatcaaa 360
 ggcactacgc ttacggtgca aacactggat tacacgttgg gacagggctg gcttgccggt 420
 aatgataccg cccacgcga ggtgaccata tatgggttca gggacctttg catggaatca 480
 aatggaggga gtgtgtgggt ggagacgtgc gtgagtagcc aaaagaacca aagatgggct 540
 ttgtacgggg atggttctat acgccccaaa caaaaccaag accaatgcct cacctgtggg 600
 agagactccg tttaacacgt aatcaatata gttagctgca gcgctggatc gtctgggcag 660
 cgatgggtgt ttaccaatga aggggccatt ttgaatttaa agaattgggt ggccatggat 720
 gtggcgcaag caaatccaaa gctccgccga ataatcatct atcctgccac aggaaaacca 780
 aatcaaatgt ggcttccgct gccagggtgga tatcactagt aaggatcc 828

<210> 4
 <211> 267
 <212> PRT
 <213> Viscum album

<400> 4
 Asp Asp Val Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly
 1 5 10 15
 Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Asp Phe Arg Asp Gly
 20 25 30
 Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
 35 40 45
 Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
 50 55 60
 Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
 65 70 75 80

Cys	Asn	Thr	Ala	Val	Arg	Glu	Ala	Thr	Leu	Trp	Gln	Ile	Trp	Gly	Asn
				85					90					95	
Gly	Thr	Ile	Ile	Asn	Pro	Arg	Ser	Asn	Leu	Val	Leu	Ala	Ala	Ser	Ser
			100					105						110	
Gly	Ile	Lys	Gly	Thr	Thr	Leu	Thr	Val	Gln	Thr	Leu	Asp	Tyr	Thr	Leu
		115					120					125			
Gly	Gln	Gly	Trp	Leu	Ala	Gly	Asn	Asp	Thr	Ala	Pro	Arg	Glu	Val	Thr
		130					135					140			
Ile	Tyr	Gly	Phe	Arg	Asp	Leu	Cys	Met	Glu	Ser	Asn	Gly	Gly	Ser	Val
145					150					155					160
Trp	Val	Glu	Thr	Cys	Val	Ser	Ser	Gln	Lys	Asn	Gln	Arg	Trp	Ala	Leu
				165					170					175	
Tyr	Gly	Asp	Gly	Ser	Ile	Arg	Pro	Lys	Gln	Asn	Gln	Asp	Gln	Cys	Leu
			180					185					190		
Thr	Cys	Gly	Arg	Asp	Ser	Val	Ser	Thr	Val	Ile	Asn	Ile	Val	Ser	Cys
		195					200					205			
Ser	Ala	Gly	Ser	Ser	Gly	Gln	Arg	Trp	Val	Phe	Thr	Asn	Glu	Gly	Ala
		210				215					220				
Ile	Leu	Asn	Leu	Lys	Asn	Gly	Leu	Ala	Met	Asp	Val	Ala	Gln	Ala	Asn
225					230				235					240	
Pro	Lys	Leu	Arg	Arg	Ile	Ile	Ile	Tyr	Pro	Ala	Thr	Gly	Lys	Pro	Asn
			245					250					255		
Gln	Met	Trp	Leu	Pro	Val	Pro	Gly	Gly	Tyr	His					
			260				265								

<210> 5
 <211> 48
 <212> DNA
 <213> Viscum album

<400> 5
 tcctctgagg tgcgctattg gccgctggtc ataaggcctg tgatagcc

48

<210> 6
 <211> 16

<212> PRT

<213> Viscum album

<400> 6

Ser Ser Glu Val Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile Ala
1 5 10 15

<210> 7

<211> 756

<212> DNA

<213> Viscum album

<400> 7

tacgaacgta tccgtctcgc tgttaccac cagaccaccg gtgaagaata tttccggttc 60
atcacgcttc tccgagatta tgtctcaagc ggaagctttt ccaatgagat accactcttg 120
cgtcagtcta cgatccccgt ctccgatgcg caaagatttg tcttgggtga gtcaccaac 180
caggggggag actcgatcac ggcgcaccac gacgttacca atctgtacgt cgtggcttac 240
caagcaggcg accaatccta ctttttgccg gacgcaccac gcggcgcgga aacgcatttc 300
ttcacgggca ccaccgata ctctctcca ttcaacggaa gctaccctga tctggagcga 360
tacgccggac atagggacca gatccctctc ggtatagacc aactcattca atccgtcacg 420
gcgcttcggt ttccggggcg cagcacgcgt acccaagctc gttcgatttt aatcctcatt 480
cagatgatct ccgaggccgc cagattcaat cccatcttat ggagggctcg ccaatacatt 540
aacagtggg cgctatttct gccagacgtg tacatgctgg agctggagac gagttggggc 600
caacaatcca cgcaagtcca gcattcaacc gatggcggtt ttaataaccc aattcggttg 660
gctatacccc ccggttaactt cgtgacgttg accaatgttc gcgacgtgat cgccagcttg 720
gcgatcatgt tgtttgtatg cggagagcgg ccatct 756

<210> 8

<211> 252

<212> PRT

<213> Viscum album

<400> 8

Tyr Glu Arg Ile Arg Leu Arg Val Thr His Gln Thr Thr Gly Glu Glu
1 5 10 15

Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly Ser
20 25 30

Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val Ser
35 40 45

Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly Asp
50 55 60

Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala Tyr

65		70		75		80
Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly Ala						
	85		90		95	
Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe Asn						
	100		105		110	
Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln Ile						
	115		120		125	
Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg Phe						
	130		135		140	
Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu Ile						
145		150		155		160
Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg Ala						
	165		170		175	
Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr Met						
	180		185		190	
Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln His						
	195		200		205	
Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro Pro						
	210		215		220	
Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser Leu						
225		230		235		240
Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro Ser						
	245		250			

<210> 9

<211> 789

<212> DNA

<213> Viscum album

<400> 9

gatgatgtta cctgcagtgc ttcggaacct acggtgcgga ttgtgggtcg aaatggcatg 60
 tgcgtggacg tccgagatga cgatttcgc gatggaaatc agatacagtt gtggccctcc 120
 aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatggaac cattcgatcc 180
 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240
 tgtaatactg ctgtgcggga ggccactctt tggcagatat ggggcaatgg gaccatcatc 300
 aatccaagat ccaatctggt ttggcagca tcatctggaa tcaaaggcac tacgcttacg 360

gtgcaaacac tggattacac gttgggacag ggctggcttg ccggtaatga taccgcccc 420
 cgcgaggtga ccatatatgg gttcaggac ctttgcattg aatcaaatgg agggagtgtg 480
 tgggtggaga cgtgcgtgag tagccaaaag aaccaaagat gggctttgta cggggatggt 540
 tctatacgcc ccaaacaaaa ccaagaccaa tgcctcacct gtgggagaga ctccgtttca 600
 acagttaatca atatagttag ctgcagcgct ggatcgcttg ggcagcgatg ggtgtttacc 660
 aatgaagggg ccattttgaa tttaaagaat gggttggcca tggatgtggc gcaagcaaat 720
 ccaaagctcc gccgaataat catctatcct gccacaggaa aaccaaata aatgtggctt 780
 cccgtgcca 789

<210> 10
 <211> 263
 <212> PRT
 <213> Viscum album

<400> 10
 Asp Asp Val Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly
 1 5 10 15
 Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Asp Phe Arg Asp Gly
 20 25 30
 Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
 35 40 45
 Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
 50 55 60
 Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
 65 70 75 80
 Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn
 85 90 95
 Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
 100 105 110
 Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
 115 120 125
 Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
 130 135 140
 Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
 145 150 155 160
 Trp Val Glu Thr Cys Val Ser Ser Gln Lys Asn Gln Arg Trp Ala Leu
 165 170 175

Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu
 180 185 190
 Thr Cys Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys
 195 200 205
 Ser Ala Gly Ser Ser Gly Gln Arg Trp Val Phe Thr Asn Glu Gly Ala
 210 215 220
 Ile Leu Asn Leu Lys Asn Gly Leu Ala Met Asp Val Ala Gln Ala Asn
 225 230 235 240
 Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro Asn
 245 250 255
 Gln Met Trp Leu Pro Val Pro
 260

<210> 11
 <211> 48
 <212> DNA
 <213> Viscum album

<400> 11
 tctcttgagg tgcgctattg gccgctgggc atacgacccg tgatagcc 48

<210> 12
 <211> 16
 <212> PRT
 <213> Viscum album

<400> 12
 Ser Ser Glu Val Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile Ala
 1 5 10 15

<210> 13
 <211> 94
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Synthetic gene
 encoding amino acids 53-78 of human P2 protein

<400> 13
gtaccgggtg gcggtcgtac cgaatccacc ttcaaaaaca ccgaaatctc cttcaaactg 60
ggtcaggaat tcgaagaaac caccgctgac aact 94

<210> 14
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Amino acids
53-78 of human P2 protein

<400> 14
Arg Thr Glu Ser Thr Phe Lys Asn Thr Glu Ile Ser Phe Lys Leu Gly
1 5 10 15
Gln Glu Phe Glu Glu Thr Thr Ala Asp Asn
20 25

<210> 15
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 20:
Synthetic linker cassette for providing modularity
at the 3' end of rMLB delta lalpha lbeta

<400> 15
caccggtaaa ccgaaccaga tgtggctgcc ggtaccgtag taacgctcot cgtcgaccta 60
gtaaggatcc ctcga 75

<210> 16
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 20: amino
acid sequence encoded by portion of SEQ ID NO: 15

<400> 16
Thr Gly Lys Pro Asn Gln Met Trp Leu Pro Val Pro

1

5

10

<210> 17

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 21:
Synthetic linker cassette for providing modularity
at the 3'end of rMLB Delta 1alpha 1beta 2gamma
with affinity module ("His-Tag").

<400> 17

ccggtaaacc gaaccagatg tggctgccgg taccgggtgg tggatatcat caccaccatc 60
accactagta actcctcgga tc 82

<210> 18

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino acid
sequence encoded by a portion of SEQ ID NO: 17

<400> 18

Gly Lys Pro Asn Gln Met Trp Leu Pro Val Pro Gly Gly Gly Tyr His
1 5 10 15

His His His His His
20

<210> 19

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Codon exchange
rMLB D23A

<400> 19

catgtgcgtg gccgtccgag atgacg

26

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 22:
Mutagenic oligonucleotides for inactivating
carbohydrate binding sites in rMLB. - 1alpha2
(W38A). -

<400> 20
cagatacagt tggcgccctc caagtcc

27

<210> 21
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 22:
Mutagenic oligonucleotides for inactivating
carbohydrate binding sites in rMLB. - 1beta (Y68S,
Y70S, Y75S, F79S). -

<400> 21
gctgcttgac cacgtctggc tctactgctg gcgtctctgt gatgatctcc gactgtaata 60
c 61

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 22:
Mutagenic oligonucleotides for inactivating
carbohydrate binding sites in rMLB. - 1beta1
(D235A). -

<400> 22
gggttggeca tggctgtggc gcaagc

26

<210> 23

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 22
Mutagenic oligonucleotides for inactivating
carbohydrate binding sites in rMLB. - 2gamma2
(Y249A). -

<400> 23
cgaataatca tcgctcctgc cacagg

26

<210> 24
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 22:
Mutagenic oligonucleotides for inactivating
carbohydrate binding sites in rMLB. - pT7 EcoRV to
SspI. -

<400> 24
cttcctttt caatattatt gaagcattta tcagg

35

<210> 25
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 22:
Mutagenic oligonucleotides for inactivating
carbohydrate binding sites in rMLB. - pT7 SspI to
EcoRV. -

<400> 25
cttcctttt cgatatcatt gaagcattta tcagg

35

<210> 26
<211> 40
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 23:
Mutagenic oligonucleotides for constructing
modular ITF gene cassettes. - pT7 Delta NdeI to
StuI. -

<400> 26

ctttaagaag gagatataca ggcctacgag aggctaagac

40

<210> 27

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 23:
Mutagenic oligonucleotides for constructing
modular ITF gene cassettes. - rMLB silent NheI. -

<400> 27

gttacctgca gtgctagcga acctacggtg cgg

33

<210> 28

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 23:
Mutagenic oligonucleotides for constructing
modular ITF gene cassettes. - rMLA Delta AgeI. -

<400> 28

cccaccagac caccggcgaa gaatatttcc gg

32

<210> 29

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Fig. 23:
Mutagenic oligonucleotides for constructing
modular ITF gene cassettes.

<400> 29
gtttgtatgc ggagagcgtc cctcgagctc tgaggtgcgc 40

<210> 30
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fig. 23:
Mutagenic oligonucleotides for constructing
modular ITF gene cassettes. - rMLB Delta EcoNI to
AgeI. -

<400> 30
ccgaataatc atcgctccgg ccaccggtaa accaaatcaa atg 43

<210> 31
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Flanking region
of the ProML gene cassette in expression vector
pT7ProML

<400> 31
tacatatgta c 11

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Flanking region
of the ProML gene cassette in expression vector
pT7ProML

<400> 32
ccatgataag gatcctctag 20

<210> 33
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Flanking region
of the IML gene cassette in expression vector
PIML-02-P

<400> 33
caggcctac

9

<210> 34
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Flanking region
of the IML gene cassette in expression vector
PIML-02-P

<400> 34
cactagtaac tctcggatc ctctagagtc gacc

34

<210> 35
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modulator
module peptide

<400> 35
Lys Asp Glu Leu
1

<210> 36
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Modulator
module peptide

<400> 36
His Asp Glu Leu
1

<210> 37
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Portion of the
ML propeptide

<400> 37
Ser Ser Ser Glu Val Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile
1 5 10 15

Ala

<210> 38
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:A degradation
product of myelin basic protein.

<400> 38
Val His Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro
1 5 10